CIFE

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HATE: * 1 1
                    RAW SEQUENCE LISTING
                                                          TIME: 14:11:41
                    FARENT AFFLI ATION: US/09/435,257B
                    ling its digit : A:\385A US.ST25.txt
                     utrut Jet: C:\CRF3\06012001\I435257B.raw
                                                                             NOV 1 3 2001
      s - 110> ABBLICANT: President and Bellia. .. Harvard College
     - FILE SEFERENCE: ARIAT HELACU
      * + 140 - CURRENT AFFILICATION NUMBER: NO - + 4 - ,2878
C--> 10 <141> CURRENT FILING DATE: 2001-05-14
     11 k160. NUMBER OF SEQ ID NOS: 34
     14 <170 | SOFTWARE: PatentIn version 3.1
                                                              ENTERED
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       211 LENGTH: 14
    18 R212 TYPE: FRT
    19 <213 - ORGANISM: Artificial Sequence
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     98 2000 TOPATTON: 011...114
    24 KU250 OTHER INFORMATION: membrane binding domain
       -kadi Seguende: 1
    29 Mot Cly For Sor Lye Ser Lys Pro Lys Asy Fro Ser Gla Arg
    31 kili seg if No: 2
    36 KU116 LENGTR: 4
    34 (111) TYPE: FRT
       0.150 0RGANISM: Artificial Sequence
       -121/ FEATURE:
    38 JUST NAME/KEY: BINDING
    59 0.270 DECATION: (1...)4
    40 k.250 OTHER INFORMATION: organize tarmeting domain
    45 (400) aBQUENCE: 2
    45 Lys Asp Glu Leu
    48 KU100 SEQ ID NO: 3
    49 K/110 LENGTH: 4
    50 kUl2: TYPE: PRT
    51 (213) OFGANISM: Artificial Sequence
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    84 KU21: NAME/KEY: BINDING
    88 <222 LOCATION: (1)..(4)
    36 Y229, OTHER INFORMATION: organized tableting domain
    19 Kijer Seguence: 3
    61 d.s Asp Glu Leu
    50h 1
    €4 <21.5 SEQ ID NO: 4
    68 K211/ LENGTH: 42
    66 BLIZE TYPE: INA
    67 KRIBO ORGANIGM: Artificial Sequence
    63 K DDI + FEATURE:
    70 < 221 > NAME REY: mlsc_structure
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71 - 222 - LOCATI N: [1 .. 42

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ng ka23> ofher information: home siming light.in
TS <400% SEQUENCE: 4
Té ogyg modomu otbyjagtota byjaddyaday yytyytyssa yb
79 +210 + 3E; ID N :
ed - 211 - DEMOTH: 41
81 KUIZ - TYPE: DNA
82 <313 - DRGANISM: Artificial Sequence
8: <220 + FEATURE:
85 KURT - NAME/WEY: misc_structure
80 KBB1 / LOCATION: (1).\overline{1}(41)
87 (323 OTHER INFORMATION: NONA BILLING DIIGU.340 9 (44) ) - SEQUENCE: 8
                                                                              41
91 atatwaatig otogagodat actggottoo aaatttoatg g
94 HALLEY SEQ IE NO: 6
95 K211 - LENGTH: 44
96 KULL TYPE: DNA
9 KMIN ORGANISM: Artificial Sequence
90 NULSON FEATURE:
190 KAAN MIME/KEY: misc structure
101 with a location: (1).\overline{\lambda}(43)
1:2 KARR CTHER INFORMATION: hCMA cloning clisc.350
105 KAUNI BEQUENCE: 6
176 atahaastog otogagtita otiggtooot toosittigti gggg
                                                                               44
109 Little SEQ ID NO:
110 K211: LENGTH: 58
111 HALL FYPE: CNA
112 -21: CEGANISM: Artificial Sequence
114 HOLDE FEATURE:
110 .M.T.: NAME/HEY: misc_structure
1.6 MR.LP LOWATION: (1)..(58)
117 HILLSH OTHER INFORMATION: hCNA cloning oligo.370
110 K4000 SEQUENCE: 7
                                                                              58
111 Beagtagggt ctagatotgg goodacgata taagtogaeg ttgaggacat ttaccage
114 K21UD SEQ ID NO: 8
115 02110 LENGTH: 9
116 HORLD TYPE: DNA
117 (213) ORGANISM: Artificial Sequence
119 KULOG FEATURE:
130 KM213 NAME/KEY: misc_structure
131 < 22.5  LOCATION: (1)..(9)
1.2 (22 %) OTHER INFORMATION: overlapping Mbal and BglII sites
135 k4000 sequence: 8
156 totacatot
159 klivy SEQ II NO: 9
140 KW11 DEMOTH: 63
   <21.6 TYPE: DNA</pre>
142 - 273 - CRRANTEM: Astrificial Requesive
144 K22UK FEATURE:
148 ×221 MAME, KEY: misb_structure
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146	R2225 Decation: (i +3)	
	<pre>%223</pre>	
	KANG KENTENTE: H	
	intiaanstaga niintisa mita niinat niitsat olinna aan ollaan olitaan ol	,: -
	eng	€3
		0.,
	<211 - LENGTH: 41	
	KO10 - TYPE: DNA	
	K213 - ORGANISM: Artificial Sequence	
	R222 - PEATURE:	
	Sud3 + OTHER INFORMATION: hONB cloning cligo.2	
	HADD SEQUENCE: 18	
		41
	atataaatog eteyagggaa atgaggeaag ttatesttty g 10 - SEQ ID NO: 11	7.1
	Hill: LENGTH: 38	
	COLOR TYPE: DNA	
	Fuls - OndanisM: Artificial Sequence	
	ALION FERTURE:	
	-1.11: NAME/KEY: misc_structure	
	+ 193+ 50CATION: (1)(38)	
	FIGURE OFFICE INFORMATION: NUMB closing uligo.3	
	+ 40GH SEQUENCE: 11	20
	indinactog Ctoyagaatg aggoaaghta toototgg	38
	F1110 F12 10 NO: 12	
	CITC LEMOTH: 65	
	- L11 - TYPE: TNA	
	+ 211- OF GANISM: Artificial Sequence	
	FEATURE:	
	+2210 NAME/HEY: misc_structure	
	+ 2220 LOCATION: (1)(65)	
	HILLER OTHER INFORMATION: hCNB/FLAG blening bligb	
	+04000 SEQUENCE: 12	
	thaatotaga totgggoodt cactigicat ogtoatotit atagiogadd adaidtadda	60
	ccatc	65
	HC10H SEQ ID NO: 13	
	+C.11: LENGTH: 116	
	HOME TYPE: DNA	
	<pre><cli>CREANISM: Artificial Sequence</cli></pre>	
	RUBOCH PEATURE:	
	HAR21H NAMEREEY: misc_structure	
	+ 022 + LOCATION: (10)116	
	KM230 OTHER INFORMATION: hCNA template linkers	
	<400> SEQUENCE: 13	
	ogatttatat gyddootota gathtagaan magaa magaa accagaacca daaccagaac	60
	हामुबब्दराबर्ष्य व व व (व (वव)) व (एवं प्रवेष्ठ वेट्टर्स प्रकार रहे गाँउ । इस्तुवि (वर्षा) व) (वर्षा)	116
	KU162 BEQ II Wit 14	
221	<2115 LENGTH: 18	

RAW SEQUENCE LISTING

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UDZ KUIZW TYPE: CNA
    -2135 GRGANISM: Applifical Sequence
210 - 1215 NAME HEY: might structure
220 + 222 + 1 7ATI N: 1 ... + f
U28 223% OTHER INF WAMATION: CNR-CNP 11:126% 0.11;0.1
231 K400% SEQUENCE: 14
232 gaatogoaaa totayatoty yqoocytoat ottiutuyno yacaccayaa olalaaso
235 <210 > SEQ ID NO: 18
237 REID - TYPE: CNA
238 k213 - ORGANISM: Artificial Sequence
040 k220 + FEATURE:
241 k221 - NAME KEY: misc_structure
242 kU22 - LOCATION: (1)..(88
243 KB2E OTHER NAPHWATTON: CMA-CMB linker clist.2
346 <400 - SEQUENCE: 15
247 gmategoada tetagatetg ggooogtoat otttatagto gasagaacsa gaassugu.
250 KM119 SEQ ID NO: 16
abl kuris LENGTH: 72
252 H212H TYPE: DNA
353 AMID ORGANISM: Artificial Sequence
255 AMADIA FEATURE:
356 × 221 × NAME/KEY: misc_signal
257 KH24 LOCATION: (1)...(72)
258 - 123 - OTHER INFORMATION: CNA 370 linker blids
261 JULE SEQUENCE: 16
PAR gyrogeticta attotaataa testagetict gyri miggit otaattotaa thotaattot
                                                                          60
284 gystataggtt st
267 KAIDS SEQ ID NO: 17
168 -0111: LENGTH: 24
269 < 1120 TYPE: PRT
270 < 1130 ORGANISM: Artificial Sequence
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273 <U210 NAME/KEY: PEPTIDE
274 < 222 LOCATION: (1) .. (24)
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278 44000 SEQUENCE: 17
280 Gly Gly Ser Gly Ser Gly Gly Ser Gly Der Gly Ser Gly Ser Gly Ser
283 Gly Mer Gly Der Gly der Gly der
284
     217 259 ID NO: 18
. 9.6
187 211 LENGTH: 01
         TYFE: DNA
2011
         PROMNICM: Artificial Caquence
         FEATURE:
   222
192 - 221 - NAMESHEY: missiteature
. 43 - 222 - DOMATIN: 1 ... 22
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- DIME: 14:11:42

Injut Jet : A:\385A US.ST25.txt atrul 3-1: C:\CRF3\06012001\I435257B.raw 294 K2235 OTHER INFORMATION: CMA primer... pan (400 / SEQUENCE: la 298 gtogacadaa bia maacaan a ٠ - -301 (210 - 3Eg 11 No: 1) 302 -211 - LENGTH: LI 303 -212 - TYFE: DNA 304 - 2132 DRGANISM: Artificial Cespence 306 -220 FEATURE: 307 <221/ NAME/KEY: mist_feature 308 KU2U LOCATION: $(1).\overline{1}(22)$ 309 KM33 DIHER INFORMATION: CNA primer.2 312 k4). Siguence: 19 313 gromadasca gaassagaas s 21 314 k21/2 SEQ ID NO: 20 317 KUIIIH LENGTH: 6 Black to server: DNA 919 <215 OFSANISM: Artificial Sequence 321 Külede FEATURE: %2210 MRME/KEY: misd feature %LDID LOTATION: (10...(6) 324 KARTH OTHER INFORMATION: Sall Site HAND SEQUENCE: 20 6 323 gwdgac 331 PUILS SEQ ID NO: 21 331 KOLIH BENGTH: 5 333 KMIMO TYPE: PRT 354 KUISH DEGANTSM: Artificial Sequence 336 KillOF FEATURE: 337 KOMIN NAME/KEY: PEPTIDE 338 KUU10 LOCATION: (1)..(5) 339 KUD3: OTHER INFORMATION: GS linker repeats 342 RADIO SEQUENCE: 21 344 Gly Gly Ser Gly Ser 345 1 347 <210> SEQ ID NO: 22 348 <211> LENGTH: 4 350 <215 OFGANISM: Artificial Sequence 350 KB260 FEATURE: 353 < 32 -> OTHER INFORMATION: mature CAP peptide fragment 355 ADRIV FEATURE: 356 <221> NAME/HEY: PEPTIDE 357 40214 bookmion: [7]../49 308 <223> OTHER INFORMATION: mature CAB iraument 361 8400% SEQUENCE: 22 363 Val Asy The Fer 361 1 individually second notices 367 - 211 - LENGTH: 6-

RAW SEQUENCE LISTING

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

HATENT ABBLINATION: US/09/435,257B

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Lift M: 841 W: 440 "h" : "Max" used, for CE, Dimit!
Lift M: 841 W: 440 "h" : "Max" used, for CE, Dimit!